

Table 1. cis-regulatory modules regulated by maternal effect and gap transcription factors and shown to be sufficient to drive domain-specific expression in blastoderm embryos.

| Gene | cis-regulatory module | Regulated by (biochemical evidence) | Regulated by (genetic evidence) | Start coord* | End coord* | CRM length | Refs. |
|---------------------|-----------------------|-------------------------------------|---------------------------------|--------------|------------|------------|-----------------|
| <i>hunchback</i> | P1 promoter | Hb, Tll | bcd, hb, tll, hkb | -4,427 | -3,006 | 1,422 | (1-7) |
| <i>knirps</i> | Upstream enhancer | Bcd, Cad, Hb, Kr, Tll | bcd, cad, hb, Kr, tll, | -2,205 | -1,177 | 1,029 | (8-11) |
| <i>Krüppel</i> | Kr730 (CD1) | Bcd, Hb, Kni, Gt, Tll | bcd, hb, kni, gt, tll | -4,331 | -3,614 | 718 | (12-15) |
| | CD2 | Gt | bcd, hb | -2,897 | -1,191 | 1,707 | (12, 15) |
| <i>even-skipped</i> | Stripe 2 | Bcd, Hb, Kr, Gt | bcd, hb, Kr, gt | -1,528 | -858 | 670 | (16-25) |
| | Stripe 3&7 | Hb, Kni | bcd, hb, kni, tll | -3,738 | -3,228 | 511 | (16-18, 26, 27) |
| | Stripe 4&6 | None | hb, kni | +4,658 | +5,259 | 602 | (28, 29) |
| | Stripe 5 | None | Kr, kni, gt | +7,401 | +8,200 | 800 | (28, 29) |
| <i>hairy</i> | Stripe 1 | None | bcd | -5,459 | -4,302 | 1,158 | (30-32) |
| | Stripe 3&4 | None | bcd, Kr, kni | -12,571 | -10,828 | 1,744 | (30-32) |
| | Stripe 5 | Kr | Kr, kni, gt | -6,022 | -5,239 | 784 | (30-32, 34) |
| | Stripe 6 | Cad, Kr, Kni | cad, hb, Kr, kni | -9,252 | -8,706 | 547 | (30-32, 34, 35) |
| | Stripe 7 | Bcd, Cad, Hb, Kr, Kni, Tll | bcd, cad, hb, Kr, kni, tll | -11,024 | -10,093 | 932 | (30-32, 35-37) |
| | Stripe 3 | None | hb, kni | -11,288 | -8,885 | 2,404 | (38-40) |
| | Stripe 5 | None | Kr, gt | -12,854 | -11,520 | 1,335 | (38-40) |
| <i>runt</i> | 7-stripe | Bcd | Bcd, tll, hkb | -5,127 | 0 | 5,128 | (38-41) |
| | Iab-2 element | Hb, Kr, Gt | hb, gt | +16,794 | +18,538 | 1,745 | (42-45) |
| <i>spalt</i> | Early enhancer | Bcd, Cad, Hb, Kr, Hkb | bcd, cad, hb, kr, hkb, tll | -10,974 | -10,459 | 516 | (7, 46) |
| <i>Ubx</i> | PBX | Hb, Tll | hb, tll | -38,735 | -38,113 | 623 | (47, 48) |

* Sequence coordinates are based on BDGP/Celera Release 1 genomic sequence and are relative to the annotated start of the transcript.

References for Table 1.

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